

## **RAW SEQUENCE LISTING** **ERROR REPORT**

BIO-TECHNICAL  
SYSTEMS  
BRANCH



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number:

09/582,779

Source:

1636

Date Processed by STIC:

1/19/2001

**THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.**

**PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:**

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT WITH A NOTICE TO COMPLY**

**FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.**

**FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.**

**PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)**

**PATENTIN 3.0 e-mail help: [patin30help@uspto.gov](mailto:patin30help@uspto.gov) or phone 703-306-4119 (R. Wax)**

**TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW.**

### **Checker Version 3.0**

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

**Checker Version 3.0 can be down loaded from the USPTO website at the following address:**

**<http://www.uspto.gov/web/offices/pac/checker>**

# Raw Sequence Listing Error Summary

## ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER:

09/582,779

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 ☐ Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line.  
This may occur if your file was retrieved in a word processor after creating it.  
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 ☐ Wrapped Aminos The amino acid number/text at the end of each line "wrapped" down to the next line.  
This may occur if your file was retrieved in a word processor after creating it.  
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 ☐ Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4 ☐ Misaligned Amino Acid Numbering The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 ☐ Non-ASCII This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.  
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 ☐ Variable Length Sequence(s) ☐ contain n's or Xaa's which represented more than one residue.  
As per the rules, each n or Xaa can only represent a single residue.  
Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.
- 7 ☐ PatentIn ver. 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) ☐. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 8 ☐ Skipped Sequences (OLD RULES) Sequence(s) ☐ missing. If intentional, please use the following format for each skipped sequence:  
(2) INFORMATION FOR SEQ ID NO:X:  
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")  
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:  
This sequence is intentionally skipped  
  
Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 ☐ Skipped Sequences (NEW RULES) Sequence(s) ☐ missing. If intentional, please use the following format for each skipped sequence.  
<210> sequence id number  
<400> sequence id number  
000
- 10 ☒ Use of n's or Xaa's, (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.  
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.  
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 ☐ Use of <213>Organism (NEW RULES) Sequence(s) ☐ are missing this mandatory field or its response.  
3-6.
- 12 ☐ Use of <220>Feature (NEW RULES) Sequence(s) ☐ are missing the <220>Feature and associated headings.  
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"  
Please explain source of genetic material in <220> to <223> section.  
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13 ☐ PatentIn ver. 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).  
Instead, please use "File Manager" or any other means to copy file to floppy disk.

1636

RAW SEQUENCE LISTING  
 PATENT APPLICATION: US/09/582,779

DATE: 01/19/2001  
 TIME: 14:17:11

Input Set : A:\ES.txt  
 Output Set: N:\CRF3\01192001\I582779.raw

**Does Not Comply  
 Corrected Diskette Needed**

OK, 3 <110> APPLICANT: Pompejus, Markus  
 4 Doval, Jose Luis Revuelta  
 5 Garcia, Maria Angeles Santos  
 7 <120> TITLE OF INVENTION: Orotidine-5'-phosphate decarboxylase gene, gene construct comprising  
 8 this gene and its use.  
 0 <130> FILE REFERENCE:  
 10 <140> CURRENT APPLICATION NUMBER: US 09/582,779  
 11 <141> CURRENT FILING DATE: 2000-07-03  
 13 <150> PRIOR APPLICATION NUMBER: Germany/19801120.2  
 14 <151> PRIOR FILING DATE: 1998-01-15  
 E--> 16 <160> NUMBER OF SEQ ID NOS: 5 (next page)  
 18 <170> SOFTWARE: WordPerfect version 6.1

# ERRORED SEQUENCES

180 <210> SEQ ID NO: 3  
 181 <211> LENGTH: 18  
 182 <212> TYPE: DNA  
 183 <213> ORGANISM: Artificial sequence  
 185 <220> FEATURE:  
 186 <221> NAME/KEY: misc\_feature  
 187 <222> LOCATION: 1 ... 18  
 W--> 189 <223> OTHER INFORMATION:  
 189 <400> SEQUENCE: 3  
 E--> 191 ynnghgncne ayathtgy  
 194 <210> SEQ ID NO: 4  
 195 <211> LENGTH: 23  
 196 <212> TYPE: DNA  
 197 <213> ORGANISM: Artificial sequence  
 199 <220> FEATURE:  
 200 <221> NAME/KEY: misc\_feature  
 201 <222> LOCATION: 1 ... 23  
 W--> 203 <223> OTHER INFORMATION:  
 203 <400> SEQUENCE: 4  
 E--> 205 taytgytgnc qaryttrtc nec  
 208 <210> SEQ ID NO: 5  
 209 <211> LENGTH: 26  
 210 <212> TYPE: DNA  
 211 <213> ORGANISM: Artificial sequence  
 213 <220> FEATURE:  
 214 <221> NAME/KEY: misc\_feature  
 215 <222> LOCATION: 1 ... 26  
 W--> 217 <223> OTHER INFORMATION:  
 217 <400> SEQUENCE: 5  
 E--> 219 tttttnatht tygargaymg naartt  
 222 <210> SEQ ID NO: 6

*Global errors*

*see item 12 on Erra Summary Sheet*

*see item 10 on Erra Summary Sheet*  
*insert cumulative base total at right margin of each line*

*same error*

*23*

*↓*



## VERIFICATION SUMMARY

PATENT APPLICATION: US/09/582,779

DATE: 01/19/2001

TIME: 14:17:12

Input Set : A:\ES.txt

Output Set: N:\CRF3\01192001\I582779.raw

L:0 M:201 W: Mandatory field data missing, FILE REFERENCE  
L:189 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:  
L:191 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3  
L:191 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:18 SEQ:3  
L:203 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:  
L:205 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4  
L:205 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:23 SEQ:4  
L:217 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:  
L:219 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5  
L:219 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:26 SEQ:5  
L:231 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:  
L:233 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6  
L:233 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:19 SEQ:6  
L:16 M:203 E: No. of Seq. differs, <160> Number Of Sequences:Input (5) Counted (6)